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piece 1, NC\_000913, eutB\_intZ+, config: linear, direction: +, begin: 2556672, end: 2556899

Sequence alignment of the 2556680, 2556690, 2556700, 2556710, 2556720, 2556730, 2556740, and 2556750 genes. The alignment shows a highly conserved sequence with several mutations highlighted by red dots.

ir eutB\_intZ+

```
{-----| p35-(23)-p10 2556697 Gap 1.4 bits  
|-----| p35-p10 2556697 total 6.2 bits
```

|-----| sd-ir 2556726 eutB\_intZ+ total 9.8 bits  
p10 2.8 bits

 p35 5.3 bits

} p35-(22)-p10 2556719 Gap 2.3 bits  
p35-p10 2556719 total 5.8 bits

**p35** 5.3 bit

~~44~~ p10 - 3 3 bits ~~1111~~ orf 35 codons

```
{ } p35-(23)-p10 2556786 Gap 1.4 bits  
p35-p10 2556786 total 7.0 bits
```

The figure displays a genomic sequence from 5' to 3' across three rows. The top row shows the sequence with start sites marked by asterisks (\*). The middle row shows the amino acid translation for each reading frame. The bottom row provides the nucleotide sequence for reference. Colored arrows above the sequence indicate transcription start sites and directionality.

{-----} sd-(10)-ir 2556880 Gap 2.7 bits  
 sd-ir 2556880 eutB\_intz+, total 5.6 bits